

Best Local Similarity 100.0%; Pred. No. 3.9e-114;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGLSTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60
DB 1 MDPARPLGLSTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60
QY 61 CROFLYGCGEGNANNFYTWACDDACWRIEKPVCRLQVSVDDQCEGSTEKYEFPNLSSM 120
DB 61 CROFLYGCGEGNANNFYTWACDDACWRIEKPVCRLQVSVDDQCEGSTEKYEFPNLSSM 120
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPCYSPKDEGLCSANTRYFFNPRY 180
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPCYSPKDEGLCSANTRYFFNPRY 180
QY 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235
DB 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

RESULT 2

AAB76856
ID AAB76856 standard; protein, 235 AA.

AC AAB76856;
DT 12-APR-2001 (first entry)

DE Human lung tumour protein related protein sequence SEQ ID NO:332.

KM Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytoskeletal; antisense inhibition.

OS Homo sapiens.

PN WO200100828-A2.

PD 04-JAN-2001.

PF 30-JUN-2000; 2000WO-US018061.

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476230.

PR 06-MAR-2000; 2000US-00519642.

PR 22-MAR-2000; 2000US-00533077.

PR 10-APR-2000; 2000US-00546259.

PR 27-APR-2000; 2000US-00560406.

PR 05-JUN-2000; 2000US-00589184.

XX (CORI-) CORIYA CORP.

PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;

PI Retter MW, Mannion J;

XX WPI; 2001-071488/08.

XX Example 1; Page 260-261; 436pp; English.

CC The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them. (I)
CC have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins

CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848
CC to AAB76878 represent human lung tumour protein related nucleotide and
CC protein sequences which are used in the exemplification of the present
CC invention

XX Sequence 235 AA;

QY Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 3.9e-114;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGLSTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60

DB 1 MDPARPLGLSTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60

QY 61 CROFLYGCGEGNANNFYTWACDDACWRIEKPVCRLQVSVDDQCEGSTEKYEFPNLSSM 120

DB 61 CROFLYGCGEGNANNFYTWACDDACWRIEKPVCRLQVSVDDQCEGSTEKYEFPNLSSM 120

QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPCYSPKDEGLCSANTRYFFNPRY 180

DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPCYSPKDEGLCSANTRYFFNPRY 180

QY 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

DB 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

RESULT 3

ABG96429
ID ABG96429 standard; protein, 235 AA.

AC ABG96429;

DT 11-DEC-2002 (first entry)

DE Human ovarian cancer marker M588.

KM Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nontuberculous granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker.

XX Homo sapiens.

PN WO200271928-A2.

PD 19-SEP-2002.

PF 14-MAR-2002; 2002WO-US007826.

PR 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-0276026P.

PR 10-AUG-2001; 2001US-0311732P.

PR 19-SEP-2001; 2001US-0323580P.

PR 26-SEP-2001; 2001US-0324967P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.

XX (MILL-) MILLENNIUM PHARM INC.

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 22, 2005, 10:02:10 ; Search time 43 Seconds
(without alignments)
407.966 Million cell updates/sec

Title: US-10-680-684-2
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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6: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	1	US-08-147-710-2
2	1306	100.0	235	1	US-08-458-090-2
3	1306	100.0	235	2	US-08-457-887-2
4	1306	100.0	235	3	US-08-817-145-3
5	1306	100.0	235	4	US-09-702-705-332
6	1306	100.0	235	4	US-09-736-457-332
7	1306	100.0	235	4	US-09-614-124B-332
8	1306	100.0	235	4	US-09-904-621-2
9	1306	100.0	235	4	US-09-671-325-332
10	1306	100.0	235	4	US-09-589-184-332
11	1306	100.0	235	4	US-09-658-824-332
12	1306	100.0	235	4	US-09-949-016-6735
13	1306	100.0	235	4	US-09-949-016-7058
14	1200	91.9	213	2	US-08-796-850-2
15	1200	91.9	213	4	US-09-766-778-2
16	394.5	30.2	291	4	US-10-000-489-48
17	393.5	30.1	291	4	US-10-000-489-52
18	388	29.7	304	1	US-08-026-145-2
19	388	29.7	304	1	US-08-446-646-9
20	388	29.7	304	1	US-08-676-125A-18
21	388	29.7	304	2	US-09-136-012A-18
22	388	29.7	304	2	US-08-676-124-1
23	388	29.7	304	3	US-08-208-264A-25
24	388	29.7	304	3	US-09-414-878-1
25	388	29.7	304	3	US-09-240-136-1
26	388	29.7	304	3	US-09-421-097-25
27	388	29.7	304	4	US-09-638-770A-1

28	388	29.7	304	4	US-09-054-272-16	Sequence 16, Appl
29	388	29.7	304	6	5466783-2	Patent No. 5466783
30	388	29.7	304	6	5466783-2	Patent No. 5466783
31	388	29.7	361	4	US-09-949-016-7400	Sequence 7400, Ap
32	387.5	29.7	276	1	US-08-437-841-9	Sequence 9, Appl1
33	387.5	29.7	276	1	US-08-286-521-9	Sequence 9, Appl1
34	387.5	29.7	276	1	US-08-436-175-9	Sequence 9, Appl1
35	387.5	29.7	276	3	US-08-854-764-3	Sequence 3, Appl1
36	387.5	29.7	276	3	US-08-943-682-9	Sequence 9, Appl1
37	387.5	29.7	276	4	US-09-741-106-9	Sequence 9, Appl1
38	387.5	29.7	276	5	PCT-US95-09377-3	Sequence 3, Appl1
39	387.5	29.7	276	5	PCT-US95-09464-9	Sequence 9, Appl1
40	384.5	29.4	213	6	5466783-25	Patent No. 5466783
41	384.5	29.4	213	6	5466783-25	Patent No. 5466783
42	384.5	29.4	276	2	US-08-796-850-1	Sequence 1, Appl1
43	384.5	29.4	276	4	US-09-766-778-1	Sequence 1, Appl1
44	384.5	29.4	277	1	US-07-844-297-1	Sequence 1, Appl1
45	384.5	29.4	352	3	US-08-854-764-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-147-710-2
; Sequence 2, Application US/08147710
; Patent No. 5455338
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Kistel, Walter
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
TITLE OF INVENTION: METHODS RELATING THERETO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,710
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 93-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-147-710-2

Query Match 100.0%; Score 1306; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1-MDPARPLGSLILFLTEAALGDAAGPTGNNATCLPLVYGPGRALLRYRYRYOS 60

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 Db 61 CROFLYGGCGEGNANNFYTWEACDCAWRIEKPVCRLQVSDVDCGSGSTKRYFENLSM 120
 Qy 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
 Db 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
 Qy 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKULRFAIRIRIKRKQF 235
 Db 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKULRFAIRIRIKRKQF 235

RESULT 2
 US-08-458-090-2
 ; Sequence 2, Application US/08458090
 ; Patent No. 5726674
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Kistiel, Walter
 ; APPLICANT: Foster, Donald C.
 ; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
 ; TITLE OF INVENTION: METHODS RELATING THERETO
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/458,090
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parker, Gary E
 ; REGISTRATION NUMBER: 31-648
 ; REFERENCE/DOCKET NUMBER: 93-14D2
 ; TELEPHONE: 206-442-6673
 ; TELEFAX: 206-442-6678
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-458-090-2

Query Match 100.0%; Score 1306; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e-123;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGILLFLTEALGDAAOEPTGNNAEICLLPLDYGPCRALRLRYYYDRYTOS 60
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 Qy 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
 Db 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
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RESULT 3
 US-08-457-887-2
 ; Sequence 2, Application US/08457887
 ; Patent No. 5914315
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Kistiel, Walter
 ; APPLICANT: Foster, Donald C.
 ; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
 ; TITLE OF INVENTION: METHODS RELATING THERETO
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/457,887
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parker, Gary E
 ; REGISTRATION NUMBER: 31-648
 ; REFERENCE/DOCKET NUMBER: 93-14D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6673
 ; TELEFAX: 206-442-6678
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-457-887-2

Query Match 100.0%; Score 1306; DB 2; Length 235;
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 Qy 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
 Db 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTI PSFCYSKDGSLCSANVTRYFENPRY 180
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RESULT 4
 US-08-817-145-3
 ; Sequence 3, Application US/08817145
 ; Patent No. 6025329
 ; GENERAL INFORMATION:
 ; APPLICANT: UTSUMI, Jun
 ; APPLICANT: SUDO, Tetsuo

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2005, 10:14:10 ; Search time 169 Seconds
(without alignments)
565.964 Million cell updates/sec

Title: US-10-680-684-2
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Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA:*

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	9	US-09-904-621-2
2	1306	100.0	235	9	US-09-736-457-332
3	1306	100.0	235	9	US-09-902-941-332
4	1306	100.0	235	9	US-09-849-626-332
5	1306	100.0	235	10	US-09-476-300-332
6	1306	100.0	235	14	US-10-017-754-332
7	1306	100.0	235	14	US-10-060-036-167
8	1306	100.0	235	14	US-10-097-340-316
9	1306	100.0	235	14	US-10-021-660-119
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12	1306	100.0	235	15	US-10-295-027-24	Sequence 24, Appl
13	1306	100.0	235	15	US-10-428-487-7	Sequence 7, Appl
14	1306	100.0	235	15	US-10-211-462-52	Sequence 52, Appl
15	1306	100.0	235	16	US-10-680-684-2	Sequence 2, Appl
16	1306	100.0	235	17	US-10-800-057-2	Sequence 2, Appl
17	1306	100.0	235	17	US-10-991-321-24	Sequence 24, Appl
18	1200	91.9	213	9	US-09-766-778-2	Sequence 2, Appl
19	1200	91.9	213	13	US-10-086-176A-6	Sequence 6, Appl
20	703.5	53.9	184	16	US-10-425-115-318379	Sequence 318379,
21	464	35.5	88	17	US-09-978-418-26	Sequence 26, Appl
22	464	35.5	88	17	US-10-485-231-26	Sequence 26, Appl
23	394.5	30.2	291	10	US-09-992-600A-48	Sequence 48, Appl
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26	394.5	30.2	291	10	US-09-999-570-48	Sequence 48, Appl
27	394.5	30.2	291	14	US-10-000-469-48	Sequence 48, Appl
28	394.5	30.2	291	14	US-10-000-986-48	Sequence 48, Appl
29	394.5	30.2	291	14	US-10-154-678-48	Sequence 48, Appl
30	394.5	30.2	291	17	US-10-838-854-48	Sequence 48, Appl
31	393.5	30.1	291	10	US-09-992-600A-52	Sequence 52, Appl
32	393.5	30.1	291	10	US-09-924-340-52	Sequence 52, Appl
33	393.5	30.1	291	10	US-09-992-095B-52	Sequence 52, Appl
34	393.5	30.1	291	10	US-09-999-570-52	Sequence 52, Appl
35	393.5	30.1	291	14	US-10-000-489-52	Sequence 52, Appl
36	393.5	30.1	291	14	US-10-000-986-52	Sequence 52, Appl
37	393.5	30.1	291	14	US-10-154-678-52	Sequence 52, Appl
38	393.5	30.1	291	17	US-10-838-854-52	Sequence 52, Appl
39	388	29.7	304	14	US-10-167-351-1	Sequence 1, Appl
40	388	29.7	304	16	US-10-755-889-412	Sequence 412, App
41	388	29.7	304	16	US-10-753-544-3	Sequence 3, Appl
42	388	29.7	304	17	US-10-931-153-1	Sequence 1, Appl
43	388	29.7	304	17	US-10-367-057-69	Sequence 69, Appl
44	388	29.7	304	18	US-10-953-902A-34	Sequence 54, Appl
45	388	29.7	304	20	US-11-083-742-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-904-621-2
Sequence 2, Application US/09904621
Patent No. US20020098560A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Kistel, Walter C.
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: AND
METHODS RELATING THERETO
FILE REFERENCE: 93-14D3
CURRENT APPLICATION NUMBER: US/09/904,621
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338
PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-621-2

Query Match 100.0%; Score 1306; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDPARPGLSILLFLTEALGDAQEPFGNNAEICLLPDPYGPCCRALTLRRYYDRYTQS 60

Qy	6	CRQFLVGGCGEANNNTYWEACDDACWRLEKXPKYCPQLQVSDQCESTTEKYFNLSM	120
Db	61	CRQFLVGGCGEANNNTYWEACDDACWRLEKXPKYCPQLQVSDQCESTTEKYFNLSM	120
Qy	121	TCEKFPSSGGCHRRINRPPDEATCMGFCAPKPIISFCYSPDDELGSANTRYENPRY	180
Db	121	TCEKFPSSGGCHRRINRPPDEATCMGFCAPKPIISFCYSPDDELGSANTRYENPRY	180
Qy	181	RTCDAAFTYTCGGDNNDNPFVSRDCCRAKCAKALAKKKKKMPKLRPFSRIPTKPKQF	235
Db	181	RTCDAAFTYTCGGDNNDNPFVSRDCCRAKCAKALAKKKKKMPKLRPFSRIPTKPKQF	235

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RESULT 2
US-09-736-457-332
Sequence 332, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chataanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121, 478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PR1
ORGANISM: Homo sapiens
US-09-736-457-332

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	Query Match	100.0%	Score 1306	DB 9	Length 235
	Best Local Similarity	100.0%	Pred. NO. 2.6e-116		
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QY	1	MDPARELGSLILLLFTEALGDAAQEPYGNNAEICLLPLDYGCRALLRYYDRYTOS	60		
Db	1	MDPARELGSLILLLFTEALGDAAQEPYGNNAEICLLPLDYGCRALLRYYDRYTOS	60		
QY	61	CHQFLYGGEGGNANFYTWACDDACMIIEKVPYCVLQVSVDDCGESTKEKFFFLSSM	120		
Db	61	CHQFLYGGEGGNANFYTWACDDACMIIEKVPYCVLQVSVDDCGESTKEKFFFLSSM	120		
QY	121	TCSEKFPSSGCHNRIENRFPDEATCMGFCAPKIKPSFCYSPKDEGLCSANVTYYNPNRY	180		
Db	121	TCSEKFPSSGCHNRIENRFPDEATCMGFCAPKIKPSFCYSPKDEGLCSANVTYYNPNRY	180		
QY	181	RKCDAPFTYGGCGDNMNFVSREDCKRAAKALKKKKKMPLRPAASRIKRIKKQF	235		
Db	181	RKCDAPFTYGGCGDNMNFVSREDCKRAAKALKKKKKMPLRPAASRIKRIKKQF	235		

RESULT 3
US-09-902-941-332
Sequence 332, Application US/09902941
Patent No. US2002017292A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Mannerakis, Margarita

```

1  APPLICANT: Carter, Darick
2  APPLICANT: Fanger, Gary R.
3  APPLICANT: Vedavick, Thomas S.
4  APPLICANT: Bangur, Chaitanya S.
5  APPLICANT: Mcnabb, Andria
6  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
7  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
8  FILE REFERENCE: 210121.478C17
9  CURRENT APPLICATION NUMBER: US/09/902,941
10 CURRENT FILING DATE: 2001-07-10
11 NUMBER OF SEQ ID NOS: 2002
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 332
14 LENGTH: 235
15 TYPE: PRT
16 ORGANISM: Homo sapiens
17 US-09-902-941-332
18
19 Query Match 100.0%; Score 1306; DB 9; Length 235;
20 Best Local Similarity 100.0%; Fred. No. 2,6e-116;
21 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db	1	MDPRPGLSLILLFLTEAALGDAQSPGTGNAIEILLPLDYGCRALLLKYVDRYQS	60
QY	61	CROFLYGCCEGNANFYTWEACDCAWRIEKVPKYLQVSVDDQCEGSTEKYEFPNLSM	120
Db	61	CROGLYGCCEGNANFYTWEACDCAWRIEKVPKYLQVSVDDQCEGSTEKYEFPNLSM	120
QY	121	TCEKFSEGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPKDEGLCSANTRYFENRY	180
Db	121	TCEKFSEGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPKDEGLCSANTRYFENRY	180
QY	181	RTCDALFYTCGGGNDNNFVSRDECKRACAALKKKKKMPKLRFAFSRIKTRKKQF	235
Db	181	RTCDALFYTCGGGNDNNFVSRDECKRACAALKKKKKMPKLRFAFSRIKTRKKQF	235

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RESULT 4
US-09-849-626-332
Sequence 332, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PR1
ORGANISM: Homo sapiens
US-09-849-626-332

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	Query Match	Best Local Similarity	Matches	Conservative	Score 1306	DB 9	Length 235	Pred. No. 2,6e-116	Mismatches	Indels	Gaps
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DB	1	1	MDPAPRPGISLILFLTEALGDPAOEPSTENNAIEICLPLPDYGCGRALLRPPYDYDRYOS	60							
QY	61		CROFLVGGCGGNANNFYWEACDCAKRIKVPVCLQVSVDDQCGSGSTEKYPFNLSM	120							

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 22, 2005, 09:59:56 / Search time 41 Seconds
(without alignments)
551.466 Million cell updates/sec

Title: US-10-680-684-2

Perfect score: 1306

Sequence: 1 MDPARPLGSHLLFLTEA.....KMPPLRFPASIRKIRKQF 235

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	2 A54951	tissue factor path
2	390	29.9	229	2 I46937	tissue factor path
3	388	29.7	304	1 TIHUGK	tissue factor path
4	384.5	29.4	304	1 JC2264	tissue factor path
5	376	28.8	302	1 TIRTKG	tissue factor path
6	372.5	28.5	300	2 S12143	lipoprotein-associ
7	346.5	26.5	396	2 S53325	tissue factor path
8	305.5	23.4	2225	2 T26063	hypothetical prote
9	303	23.2	2167	2 T34395	hypothetical prote
10	299	22.9	1965	2 T33216	hypothetical prote
11	292.5	22.4	1558	2 C89114	protein C37C3.6a l
12	285	21.8	922	2 T23573	hypothetical prote
13	279.5	21.4	1522	2 H88380	protein T22F7.3 i
14	271.5	20.8	1416	2 E88550	protein ZC84.1 l
15	268	20.5	1474	2 D88550	protein ZC84.6 l
16	268	20.5	1474	2 D88550	protein ZC84.6 l
17	268	20.5	1474	2 D88550	protein ZC84.6 l
18	253.5	19.4	1043	2 T19734	hypothetical prote
19	252	19.3	1743	2 T26859	hypothetical prote
20	250	18.4	1391	2 T20406	hypothetical prote
21	239	18.3	838	2 T20125	hypothetical prote
22	215	16.5	252	2 JG0185	hepatocyte growth
23	215	16.5	1208	2 T27822	hypothetical prote
24	214	16.4	352	2 T1BOBI	alpha-1-microglobu
25	206	15.8	1203	2 T21275	hypothetical prote
26	199	15.2	692	2 T32960	hypothetical prote
27	197	15.1	228	2 T20219	hypothetical prote
28	196	15.0	123	2 A29652	inter-alpha-trypsi
29	191	14.6	337	1 T1PGBI	alpha-1-microglobu

30	188	14.4	183	2 T28711	hypothetical prote
31	186	14.2	125	1 T1BOBI	alpha-1-microglobu
32	186	14.2	349	2 S21089	alpha-1-microglobu
33	184.5	14.1	359	2 S35708	gamma-1-microglobu
34	182.5	14.0	355	1 S22181	alpha-1-microglobu
35	180	13.8	352	1 HCHU	hypothetical prote
36	178.5	13.7	502	2 T20130	hypothetical prote
37	174	13.3	61	1 T1VTR1	venom basic prote
38	173	13.2	335	2 T32657	hypothetical prote
39	172	13.2	62	2 S19327	venom basic prote
40	168	12.9	62	2 S07451	proteinase inhibit
41	166.5	12.7	372	2 JC2556	alpha-1-microglobu
42	165.5	12.7	110	1 T1TVOR	basic proteinase i
43	165	12.6	65	1 T1VIVC	venom basic protei
44	164	12.6	265	2 A53390	Kunitz-type protei
45	163	12.5	57	2 A59204	basic proteinase i

ALIGNMENTS

10/1/1993

RESULT 1
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A54951
N/Alternate names: placental protein 5 (PP5)
C/Species: Homo sapiens (man)
C/Date: 31-May-1996 #sequence revision 31-May-1996 #text change 09-Jul-2004
C/Accession: A54951; 155185; A34029; C34029; B34029
R/Sprecher, C.A.; Kistel, W.; Mathewes, S.; Foster, D.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994
A/Title: Molecular cloning, expression, and partial characterization of a second human
A/Reference number: A54951; MUID:94211862; PMID:8159751
A/Accession: A54951
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-235 <RES>
A/Cross-references: UNIPROT:P48307; GB:L27624; NID:G441149; PIDN:AAA20094.1; PID:G44115
A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
A/Accession: A34029
A/Molecule type: protein
A/Residues: 1-235 <RES>
A/Cross-references: GB:D29992; NID:G484050; PIDN:BA06272.1; PID:G484051
A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
A/Accession: A34029
A/Molecule type: protein
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
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Biochem. Biophys. Res. Commun. 150, 483-490, 1988
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A/Accession: A34029
A/Molecule type: protein
A/Residues: 1-235 <RES>
A/Cross-references: GB:D29992; NID:G484050; PIDN:BA06272.1; PID:G484051
A/Note: parts of this sequence, including the amino end of the mature protein, were det
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A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
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Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
A/Accession: A34029
A/Molecule type: protein
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
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A/Title: Purification and characterization of placental protein 5.
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A/Accession: A34029
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
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R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
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A/Cross-references: GB:D29992; NID:G484050; PIDN:BA06272.1; PID:G484051
A/Note: parts of this sequence, including the amino end of the mature protein, were det
R/Buetzow, R.; Huhntala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
A/Accession: A34029
A/Molecule type: protein
A/Residues: 1-235 <RES>
A/Cross-references: GB:D29992; NID:G484050; PIDN:BA06272.1; PID:G484051
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A/Note: parts of this sequence, including the amino end of the mature protein, were det
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A/Accession: A34029
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Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A/Title: Purification and characterization of placental protein 5.
A/Reference number: A34029; MUID:88106628; PMID:3276312
A/Accession: A34029
A/Molecule type: protein
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RESULT 2
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C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: I46937
R:Belalouaj, A.; Kumpusamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A/Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A/Reference number: I46937; MUID:93276427; PMID:8503123
A/Accession: I46937
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-299 <BEL>
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C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BFI1>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BFI2>
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RESULT 3
TIHUCK
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N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A28294; S03903

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R:Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; Macphail, L.A.; Likert, K.M.; Byers, M.G.
J. Biol. Chem. 266, 5036-5041, 1991
A/Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intr
A/Reference number: A23712; MUID:91161593; PMID:2002045
A/Accession: A23712
A/Molecule type: DNA
A/Residues: 1-304 <GIR>
A/Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:9187204; PIDN:AA59526.1;
Biochemistry 30, 1571-1577, 1991
A/Title: Intron-exon organization of the human gene coding for the lipoprotein-associate
A/Reference number: A39176; MUID:91129227; PMID:1993173
A/Accession: A39176
A/Molecule type: DNA
A/Residues: 1-304 <VAN>
A/Cross-references: GB:M58650; GB:J05312; NID:9186827; PIDN:AA59480.1; PID:9186829
R:Wu, T.C.; Kretzmer, K.R.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 263, 6001-6004, 1988
A/Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated cc
A/Reference number: A28650; MUID:88198127; PMID:2452157
A/Accession: A28650
A/Molecule type: mRNA
A/Residues: 1-304 <G12>
A/Cross-references: GB:J03225; NID:9180545; PIDN:AA52022.1; PID:9180546
A/Note: part of this sequence, including the amino end of the mature protein, was confir
R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.
Thromb. Res. 55, 37-50, 1989
A/Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated
A/Reference number: A60433; MUID:89388722; PMID:2781520
A/Accession: A60433
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-304 <G12>
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A/Accession: B60433
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A/Residues: 'XX', 31-53, 'X', 55-56 <G13>
A/Experimental source: recombinant material from mouse C137 cells
R:Girard, T.J.; McCourt, D.; Novotny, W.F.; Macphail, L.A.; Likert, K.M.; Broze Jr., G.J.
Biochem. J. 270, 621-625, 1990
A/Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor
A/Reference number: S13034; MUID:91054349; PMID:2122883
A/Accession: S13034
A/Molecule type: protein
A/Residues: 29-35 <G14>
R:Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 264, 18832-18837, 1989
A/Title: Purification and characterization of the lipoprotein-associated coagulation inh
A/Reference number: A34315; MUID:90036996; PMID:2553722
A/Accession: A34315
A/Molecule type: protein
A/Residues: 'XX', 31-33, 'L', 35-50 <NOV>
A/Experimental source: plasma
R:Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
J. Biol. Chem. 265, 16786-16793, 1990
A/Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and chara
A/Reference number: A38294; MUID:91009092; PMID:2211593
A/Accession: A38294
A/Molecule type: protein
A/Residues: 29-41 <PED>
R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.;
Nature 338, 518-520, 1989
A/Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as
A/Reference number: S03903; MUID:89181950; PMID:2927510
A/Contents: annotation; site-directed mutagenesis
C/Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
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A/Genes: GDB:TFPI
A/Cross-references: GDB:127364; OMIM:152310
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A/Intons: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
C/Function:
A/Description: regulates clotting by factor Xa-dependent inhibition of the coagulation f

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 09:36:09 ; Search time 172 Seconds
(without alignments)
699,643 Million cell updates/sec

Title: US-10-680-684-2

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1231.5	94.3	224	2 Q8NAK6	Q8NAK6 homo sapien
3	943	72.2	167	2 Q8NR89	Q8NR89 homo sapien
4	939.5	71.9	234	2 Q7YR08	Q7YR08 bos taurus
5	654	50.1	230	2 Q8CF99	Q8CF99 rattus norv
6	644	49.3	230	1 TFP2 MOUSE	Q35536 mus musculu
7	635	48.6	224	2 Q7T0Z5	Q7T0Z5 xenopus lae
8	388	29.7	304	1 TFP1 HUMAN	P10646 homo sapien
9	387.5	29.7	300	1 TFP1 RABIT	P19761 oryctolagus
10	387	29.6	287	2 Q93424	Q93424 cyprinus ca
11	384.5	29.4	304	1 TFP1 MACMU	Q28864 macaca mula
12	378	28.9	306	1 TFP1 MOUSE	Q54819 mus musculu
13	376	28.8	302	1 TFP1 RAT	Q02445 rattus norv
14	367.5	28.1	279	2 Q7Z4Z2	Q7Z4Z2 brachydanio
15	361	27.6	241	2 Q7PKX1	Q7PKX1 anopheles g
16	358.5	27.5	759	2 Q8I791	Q8I791 ancylostoma
17	357.5	27.4	3198	2 Q9U8G8	Q9U8G8 manduca sex
18	346.5	26.5	396	2 Q28874	Q28874 canis fami
19	336.5	25.8	2772	2 Q9VAV4	Q9VAV4 drosophila
20	336.5	25.8	2776	2 Q86940	Q86940 drosophila
21	336.5	25.8	2894	2 Q7KRX2	Q7KRX2 drosophila
22	336.5	25.8	2898	2 Q86829	Q86829 drosophila
23	325	24.9	1572	2 Q44938	Q44938 drosophila
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27	303	23.2	2167	2 Q76840	Q76840 caenorhabdi
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34	279.5	21.4	988	2 Q22685	Q22685 caenorhabdi
35	276	21.1	277	2 Q8AYE1	Q8AYE1 brachydanio
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42	268	20.5	507	2 Q9D3K4	Q9D3K4 mus musculu
43	268	20.5	507	2 Q99J04	Q99J04 mus musculu
44	268	20.5	1474	2 Q62504	Q62504 caenorhabdi
45	268	20.5	1599	2 Q09983	Q09983 caenorhabdi

ALIGNMENTS

RESULT 1
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AC P48307
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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GN Name=TFPI2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=95204397; PubMed=7896752;
RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F., Aoki I., Mitsu K., Umeda M., Miyazaki K.;
RT "CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by cancer cells: identification as placental protein 5 and tissue factor pathway inhibitor-2.";
RT J. Biochem. 116:939-942(1994).
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RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94211862; PubMed=8159751;
RA Sprecher C.A., Kistiel W., Mathews S., Foster D.C.;
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RN [3]
RP SEQUENCE FROM N.A.
RA Maggi L.;
RT Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Steapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Frange C.,

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 RA Bosnak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gamarate P.H.,
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 RA Vallotton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Hahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalske U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
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 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
 RC TISSUE=Placenta;
 RX MEDLINE=88106628; PubMed=3276312;
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppälä M.;
 RT "Purification and characterization of placental protein 5.";
 RL Biochem. Biophys. Res. Commun. 150:483-490(1988).
 RN [7]
 RP ERRATUM.
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppälä M.;
 RL Biochem. Biophys. Res. Commun. 151:630-631(1988).
 CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,
 CC weakly factor Xa. Has no effect on thrombin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,
 CC placenta, heart, pancreas, and maternal serum at advanced
 CC pregnancy.
 CC -1- DOMAIN: This inhibitor contains three inhibitory domains.
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; D29992; BA06272.1; -;
 DR EMBL; L27624; AAA20094.1; -;
 DR EMBL; AC002076; AAS02022.1; -;
 DR EMBL; AF217542; AAK13254.1; -;
 DR EMBL; BC005330; AA05330.1; -;
 DR PIR; A54951; A54951.
 DR HSSP; P10646; 11RH.
 DR Genew; HGNC:11761; TFP12.
 DR H-InVDB; HIX0006849; -;
 DR MIM; 600033; -;
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR InterPro; IPR002223; Prot. Inh_Kunz-m.
 DR InterPro; IPR008296; TFP1.
 DR Pfam; PF00014; Kunitz BPTI; 3.
 DR PIRSF; PIRSF01620; TFP1; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Prot. Inh_Kunz-m; 3.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
 KW Blood coagulation; Direct protein sequencing; Glycoprotein;
 KW Polymorphism; Repeat; Serine protease inhibitor; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 235 Tissue factor pathway inhibitor 2.
 FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 96 149 BPTI/Kunitz inhibitor 2.
 FT DOMAIN 158 208 BPTI/Kunitz inhibitor 3.
 FT DOMAIN 213 217 POLY-Iivs.
 FT SITE 46 47 Reactive bond (By similarity).
 FT SITE 107 108 Reactive bond (By similarity).
 FT SITE 168 169 Reactive bond (By similarity).
 FT DISULFID 36 86 By similarity.

FT DISULFID 45 69 By similarity.
 FT DISULFID 61 82 By similarity.
 FT DISULFID 96 149 By similarity.
 FT DISULFID 106 130 By similarity.
 FT DISULFID 122 145 By similarity.
 FT DISULFID 158 208 By similarity.
 FT DISULFID 167 191 By similarity.
 FT DISULFID 183 204 By similarity.
 FT CARBOHYD 116 116 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 170 170 N-linked (GlcNAc...) (potential).
 FT VARIANT 102 102 V -> A (in dbSNP:1804202).
 FT VARIANT 102 102 /FTID=VAR_012005.
 FT CONFLICT 23 23 D -> A (in Ref. 6).
 SQ SEQUENCE 235 AA; 26934 MW; 975BA5C53F7C65F CRC64;
 Query Match 100.0%; Score 1306; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e-110; Indels 0; Gaps 0;
 Matches 235; Conservative 0; Mismatches 0;
 QY 1 MDPARPLGSLILLFTLEALGDAQEPYNNALICLLPLDYGPCRALLRYYDRYTOS 60
 DB 1 MDPARPLGSLILLFTLEALGDAQEPYNNALICLLPLDYGPCRALLRYYDRYTOS 60
 QY 61 CROFLYGCCEGNANFYWEACDDACWRIEYKPKVCRLQVSYDDQCEGSTEYFNLSSM 120
 DB 61 CROFLYGCCEGNANFYWEACDDACWRIEYKPKVCRLQVSYDDQCEGSTEYFNLSSM 120
 QY 121 TCCEFFSGGCHNRIRNRPDPATCWCPCAPKKIBPFCYSPDEGICSNANTRYNPRY 180
 DB 121 TCCEFFSGGCHNRIRNRPDPATCWCPCAPKKIBPFCYSPDEGICSNANTRYNPRY 180
 QY 121 TCCEFFSGGCHNRIRNRPDPATCWCPCAPKKIBPFCYSPDEGICSNANTRYNPRY 180
 DB 121 TCCEFFSGGCHNRIRNRPDPATCWCPCAPKKIBPFCYSPDEGICSNANTRYNPRY 180
 QY 181 RTCDATYTGCGGNDNPFVSRDCRCAKALKKKKPKLFPASIRIRIKKQF 235
 DB 181 RTCDATYTGCGGNDNPFVSRDCRCAKALKKKKPKLFPASIRIRIKKQF 235
 RESULT 2
 Q8NNA6 PRELIMINARY; PRT; 224 AA.
 AC Q8NNA6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira T., Kikawa E., Omura Y.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimura K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe M., Hosoda M., Hotta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshioka S., Matsumawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,